GCCATCCCAT CAACAGAAGG TTTAAGTGGA AATCCATTTC ATTAGAAAG   50

ATCGGACAAA GGGTACTCTT AAGCATACAA C ATG AGG GCG GTG GCG   96
                                       Met Arg Ala Val Ala
                                           5

GTT TTT GCT TGC GTT CTC TTC TGT ATG GTT CAC AAA GCC   138
Val Phe Ala Cys Val Leu Phe Cys Met Val His Lys Ala
          10   15

GCA CTT GCG GAT GAT AAA ACG TGC AAC CCT ACA GAT TTT ATG   180
Ala Leu Ala Asp Asp Lys Thr Cys Asn Pro Thr Asp Phe Met
        20   25   30

GTT ACC CAA ACC ATA ACT GGA TTG ACA ATC GGC GGT AAA CAA   222
Val Thr Gln Thr Ile Thr Gly Leu Thr Ile Gly Gly Lys Gln
        35   40   45

GAG TTC GAG GTC AAT TTA ATA AAC AAT TTG TAT TGT GCA CAA   264
Glu Phe Glu Val Asn Leu Ile Asn Asn Leu Tyr Cys Ala Gln
        50   55   60

A - A

FIG. 1a

A ---

```
TCT AAT GTC AAA GTT TCA TGT GAC GGG CTT CAT ACC ACC GAA   306
Ser Asn Val Lys Val Ser Cys Asp Gly Leu His Thr Thr Glu
        65                      70                    75

CCA ATA GAT CCT CAC ATT ATC AGA CCA CTT AGT GAC GGA ACG   348
Pro Ile Asp Pro His Ile Ile Arg Pro Leu Ser Asp Gly Thr
                 80                     85

AAC AAC TGC CTT GTC AAC AAT GGA GCG CCT ATT TCT CAT GCT   390
Asn Asn Cys Leu Val Asn Asn Gly Ala Pro Ile Ser His Ala
 90                     95                    100

ACT CTT GTA GCA TTC AAG TAT GCC TGG GAT GTT CCT CCA TCT   432
Thr Leu Val Ala Phe Lys Tyr Ala Trp Asp Val Pro Pro Ser
105                    110                   115

TTC AGC ATC ATC AGC TCT GAT ATA AAT TGC TCC TAA   468
Phe Ser Ile Ile Ser Ser Asp Ile Asn Cys Ser OCH
120                    125

GGAGAAA ATTCTAGTTG GCAGAGAATA ATCATATAGT CTTTTTTACT   515
```

B ---

FIG. 1b

B - - · - · - · - · - · - · - · - · - · - · - · - · - · - · - - B

GAGCTATTTA ATTTTTTCAA TTTTCACCAA TAAGATTATT TTAATGGAAT 565

GTTAATGTAT TAGAATTGAA AAATAAAAAA AAAAAAAAAA AAAAAAAAA 615

AAAAAAAAAA 625

FIG. 1c

```
                                                                    48
GAAAGTTGAA ACATCTCCAT CAAACTCTAG AGTCAGATTT CCCACAAG

                                                                    87
ATG ATT TCA TCG GCA AAT AAC AAA GGC GCC GGC ACA AGC
Met Ile Ser Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser
                  5                    10

                                                                   126
CGC CGC AAG CTC CGT TCT GAG AAG GCT GCA CTC CAG TTC
Arg Arg Lys Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe
           15                   20                25

                                                                   165
TCC GTC AGT CGC GTC GAA TAC TCC CTC AAG AAG GGG CGC
Ser Val Ser Arg Val Glu Tyr Ser Leu Lys Lys Gly Arg
                30                   35

                                                                   204
TAT TGC AGG CGC TTA GGC GCT ACG GCC CCC GTC TAC CTA
Tyr Cys Arg Arg Leu Gly Ala Thr Ala Pro Val Tyr Leu
     40                   45                   50

                                                                   243
GCC GCC GTC CTT GAA AAC CTC GTG GCC GAA GTG TTG GAC
Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp
                55                   60                65
```
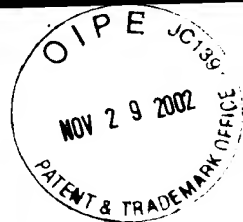
FIG. 5a

A - - - - - - - - - - - - - - - - - A

```
ATG GCG GCG AAC GTG ACA GAA GAA ACA TCC CCC ATT GTT   282
Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val
    70                              75

ATC AAA CCG AGG CAT ATT ATG CTT GCC CCC AGG AAT GAT   321
Ile Lys Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp
        80                      85                  90

GTA GAA GTT GAA CAA GCT GTT TCA CGG TGT CAC CAT CTC   360
Val Glu Val Glu Gln Ala Val Ser Arg Cys His His Leu
            95                          100

GGC ATC AGG TGT CGT CCC TAAAAACACGC AAAGAGCTGG        398
Gly Ile Arg Cys Arg Pro
105                 110

ACCGTCGCAA ACGCCGTTCC ACCTTTCAGC CGGATTAGTT CTTGATATTT  448

CATTCTATCA ATCTTGGTTA TGTGACTGTG ATTTTTCGTT TTGTGTTGAA  498
```

B - - - - - - - - - - - - - - - - - B

FIG. 5b

B - - - - - - - - - - - - - - - - - - B

```
CTAAGCCCCC TAATCTGGAT TTCTCGTTTT ATGTTGAACT AAGTCTGTGC   548
ACTCTTGAAG TAAAAAAAAA AAAAAAAAAA AAAAAAAA              587
```

FIG. 5c

GATCCCAAAT CATCA ATG ACG ATC CCC GAA AAG AAA TCC GTC 42
          Met Thr Ile Pro Glu Lys Lys Ser Val
          1   5

GCT CCG ATG GCC CGT ATG AAG CAT ACA GCC CGC ATG TCT 81
Ala Pro Met Ala Arg Met Lys His Thr Ala Arg Met Ser
10   15   20

ACC GGC GGT AAG GCT CCA CGC AAG CAG CTC GCC TCT AAG 120
Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Ser Lys
        25   30   35

GCT CTT CGC AAG GCG CCA CCA CCG ACC AAA GGA GTG 159
Ala Leu Arg Lys Ala Pro Pro Pro Thr Lys Gly Val
            40   45

AAG CAG CCC ACC ACT ACC TCC GGA AAA TGG CGC TTC 198
Lys Gln Pro Thr Thr Thr Ser Gly Lys Trp Arg Phe
        50   55   60

FIG. 6a

A

GCG AGA TTT CAC AGG AAA CTG CCA TTC CAA GGG CTG GTG
Ala Arg Phe His Arg Lys Leu Pro Phe Gln Gly Leu Val   237
            65   70

AGG AAA ATC TGG CAG GAC TTG AAG ACA CAT CTG CGC TTC
Arg Lys Ile Trp Gln Asp Leu Lys Thr His Leu Arg Phe   276
        75   80   85

AAG AAC CAC TCG GTT CCT CCA CTT GAG GAG GTA ACT GAG
Lys Asn His Ser Val Pro Pro Leu Glu Glu Val Thr Glu   315
            90   95   100

GTT TAT CCT TGC CAA ACT ATT GGA GGA TGC TAT
Val Tyr Pro Cys Gln Thr Ile Gly Gly Cys Tyr   348
            105

TAGGATATTG AATTTGGATA ATGGTTTAAT TATCTGTTCT ACCTTTATGA   398

TCAAATTTCT GTGGCTCAGC GTTGTGTAAT TTGGGCAATC GAATTCTTAG   448

CTATATTGCC TCAAAAAAAA AAAAAAAAA AAAAAAA   485
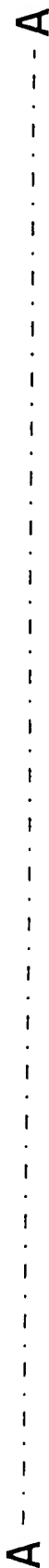
FIG. 6b

```
GGAGGGTGTT  GGAATTAGGT  TTGCCTAGGG  TTGCCTAGG   TTTAGAGAAA   50
TAGTCAAAAT  TGTCCTATTC  TATAGGCATG  ATTTAGTAGT  GAGTTAATTA  100
TCCTATAATT  TCTCTTCTTG  TATGCTCAAA  TAACTGGTTC  TTTAATGAAT  150
AGATAATTAA  GTTTGTAGC   AATTCTTCC   TCAAATTGAG  TATCAACAAT  200
TGTTAGATTG  CTTTGGTGAT  TATATTTGAT  ATAATTGTTT  GTAAGAATGT  250
GTAGTGAAAA  GATTGTGATT  ATTCATTTCG  TTGTTGGACG  AATTGTTAGA  300
GCCCCATCGC  TAATGCCTTA  TAGTACTCGA  AATATGTTGG  GAATAGAAGA  350
TGAAAAATCC  CATTCTTTGT  AGTAGGAGTA  AAAATTGTC   TTTTCATTAT  400
TCCATTGAAT  GTTAACCACT  TGCCATTCAT  CTGACGGGGA  TGGCAGAGTT  450
CCGACCATCT  AGTGATCCGT  GGGATATTGA  TTTGGTGTG   TCAATGAAAT  500
TGTGAGAACG  GGCTTCTGGG  AGAGAAAAGC  CCTCTTGCCT  CTGATATGAA  550
CACTGAGGCT  GATTATGTTA  ACGGATGGAG  ATTTATCAGT  GGCTGAATTT  600
GGGTGCTGTA  GAGACAGAAT  TTGAAAGTTC  TAACAATAAA  CCCTAATTCT  650
GAACTTGGGC  GGGGCTGGGA  TTTTACTCTT  AACGTGAAGA  GAGGCAAGAT  700
GAATTGACAG  CTTGGAAGTC  GATCCAGTAT  TTGCAGCAGT  CGTGACGAAT  750
```

A - - - - - - - - - - - - - - - - - - - A

FIG. 10a

A ------------------------------- A

TGGTTGGACA GTTACATCGG TCAGAGAATG CGTTCTATAA ATTCCCCCAA   800

TGCGGCAGTG AAAATCCCAT CCCATCAACA GAAGTTTTAA GTGGAAACCC   850

ATTCCAATAG AGAAGATCGA ACAAAGGGTA TTTAAACATA CAAATGGGGG   900

CAGTGGGTGTT TCTTTTTGCT TGCGTTCTCT TCTGTATGGT TCACA   945

FIG. 10b